

Wed May 9 10:10:02 2001

us-09-673-779-1.rge

Db 293 GCCTGCCAGTTTGCATG 276

RESULT 10
STY426/c 326 bp DNA BCT 04-FEB-1999
DEFINITION
S. typhi DNA.
ACCESSION
D12813.1 GI:303923
VERSION
D12813.1 GI:303923
KEYWORDS
Salmonella typhi DNA.
SOURCE
Salmonella typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.

REFERENCE
1 (sites)
Iida, K., Abe, A., Matsui, H., Tanbara, H., Wakayama, S. and Kawahara, K.
Rapid and sensitive method for detection of salmonella strains
using a combination of polymerase chain reaction and reverse
dot-blot hybridization.
FEMS Microbiol. Letters 114, 167-172 (1993)

JOURNAL
AUTHORS
Iida, K.
Unpublished (1994)
Submitted (04-Aug-1992) to DDBJ by:
Kazuo Iida
Research and Development
Kibun Foods Inc.
Ginza 7-14-13
Chuo-ku Tokyo 104
Japan
Phone: 03-3544-2754
Fax: 03-3545-0860.

FEATURES
source
1..326
/organism="Salmonella typhi"
/db_xref="taxon:601"

BASE COUNT
81 a 71 c 108 g 66 t

Query Match 100.0%; Score 18; P=1e-4; Length 326;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gcttcgcaattcgatg 18
|||||
Db 293 GCCTGCCAGTTTGCATG 276

RESULT 11
STY426/c 326 bp DNA BCT 04-FEB-1999
DEFINITION
S. typhimurium DNA.
ACCESSION
D12814
VERSION
D12814.1 GI:303924
KEYWORDS
Salmonella typhimurium (strain:IT2) DNA.
SOURCE
Salmonella typhimurium
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Salmonella.

REFERENCE
1 (sites)
Iida, K., Abe, A., Matsui, H., Tanbara, H., Wakayama, S. and Kawahara, K.
Rapid and sensitive method for detection of salmonella strains
using a combination of polymerase chain reaction and reverse
dot-blot hybridization
FEMS Microbiol. Letters 114, 167-172 (1993)

JOURNAL
AUTHORS
Iida, K.
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Ginza 7-14-13
Chuo-ku Tokyo 104
Japan
Phone: 03-3544-2754
Fax: 03-3545-0860.
FEATURES
source
1..326
/organism="Salmonella typhimurium"
/strain="IT2"
/db_xref="taxon:601"

Query Match 100.0%; Score 18; P=1e-4; Length 326;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0;

QY 1 gcttcgcaattcgatg 18
|||||
Db 293 GCCTGCCAGTTTGCATG 276

RESULT 12
BSPX91531/c 347 bp DNA BCT 17-SEP-1995
DEFINITION
Bacterial sp. partial 16S rRNA gene (clone: group K16)
ACCESSION
X91531
VERSION
X91531.1 GI:987806
KEYWORDS
16S ribosomal RNA; 16S rRNA gene
SOURCE
unidentified bacterium.
unidentified bacterium.
Bacteria; environmental microorganisms

REFERENCE
1 (bases 1 to 347)
AUTHORS
Pedersen, K.
Unpublished
TITLE
Direct Submission
JOURNAL
Submitted (13-SEP-1995) K. Pedersen, Dan Herq Institut
and Marine Microbiology, Medicinertan 9 E, 4130
SWELEN

FEATURES
source
1..347
/organism="unidentified bacterium"
/isolate="clone group K16"
/db_xref="taxon:2338"

RNA
<1..347
/gene="16S rRNA"
/product="16S ribosomal RNA"

gene
1..347
/gene="16S rRNA"

BASE COUNT
85 a 75 c 113 g 65 t 9 others

Query Match 100.0%; Score 18; P=1e-4; Length 347;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0;

QY 1 gcttcgcaattcgatg 18
|||||
Db 116 GCCTGCCAGTTTGCATG 99

RESULT 13
AF181899/c 408 bp DNA BCT 07-DEC-1997
LOCUS
AF181899
DEFINITION
Uncultured bacterium clone: dd/1 16S ribosomal RNA gene
sequence.

```

LOCUS      VIB1293     181 bp     rRNA
DEFINITION Vibrio cholerae 12S rRNA.
ACCESSION D1293
VERSION   011293.1 GI:560123
KEYWORDS  16S rRNA.
SOURCE    Vibrio cholerae
ORGANISM  Vibrio cholerae
REFERENCE 1 (bases 1 to 181)
AUTHORS  Kita-Tsukamoto, K.
TITLE    Direct Submission
JOURNAL   J. Biol. Chem. 267:1336-1340, 1992
PUBMED    1311143 (20 APR 1992)
KITA-TSUKAMOTO, K. Department of Microbiology, Faculty of Medicine, University of Tokyo, Yonsei Kaikan Bldg. 1F-15-1 Minamida 1, Nakano-ku, Tokyo 164, Japan.
E-MAIL   tsukamoto@a13.ori.u-tokyo.ac.jp Tel: 03-5455-5111 Fax: 03-5375-6716
2 (bases 1 to 181)
AUTHORS  Kita-Tsukamoto, K., Ogaichiro, N., Kato, K. and Shimidzu, T.
TITLE    Phylogenetic relationships of marine bacteria, mainly the family Vibrionaceae, determined on the basis of 16S sequences
JOURNAL   Int. J. Syst. Bacteriol. 41(1):1-10 (1991)
PUBMED    93152464
MEDLINE   93152464
COMMENT   Cl Oct 27, 1994 this sequence location replaced location 1.181
FEATURES  location/Qualifiers
           1..181
           /organism="Vibrio cholerae"
           /db_xref="taxon:1293"
BASE COUNT 50 a 42 c 50 g
ORIGIN

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DB	29	GIACCCTACCTCGTAAGG 12	RESULT 3
LOCUS	VIB16SR09/c		
DEFINITION	Vibrio parahaemolyticus 16S rRNA.		
ACCESSION	D11314		
VERSION	D11314.1	GI:287465	
KEYWORDS			
SOURCE			
ORGANISM	Vibrio parahaemolyticus (strain 01-170c) RNA.		
REFERENCE	Vibrio parahaemolyticus Bacteria, Proteobacteria; Gamma subdivision; Vibrionales (bases 1 to 190)		
AUTHORS	Kita-Isukamoto,K		
TITLE	Direct Submission		
JOEPMAL	Submitted (35-APR-1995) to the EMBL/GenBank/Joint Genome Center, University of Tokyo, Ocean Research Institute, 1-15-1 Minamiohara, Nakano-Ku, Tokyo 164, Japan. (E-mail: tukamoto@ai3.cri.tyohoku.ac.jp) Tel:03-3375-6716 Fax:03-3375-6716)		
REFERENCE	2. (bases 1 to 190)		
AUTHORS	Kita-Isukamoto,K; Oyazaki,H; Nakano,K; and Shimada,T		
TITLE	Phylogenetic relationships of marine bacteria, mainly the family Vibrionaceae, determined on the bases of 16S sequences		
JOURNAL	Int. J. Syst. Bacteriol. 43 (1993) 1943		
MEDLINE	93152464		
FEATURES	Location/Qualifiers		
source	1..190		
	/organism="Vibrio parahaemolyticus"		
	/strain="ATCC17902"		
	/db_xref="taxon:670"		
BASE COUNT	53 a 46 c 54 g 47 t 1 others		
ORIGIN			

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us-09-673-779-3.rge

12 100.0 1144 1 AF076037
13 100.0 1149 1 AF076038
14 100.0 1185 1 AF076039
15 100.0 1417 2 ECERNH3
16 100.0 1418 2 ECERNH3
17 100.0 1418 2 ECERNH3
18 100.0 1436 2 ECERNH3
19 100.0 1436 2 ECERNH3
20 100.0 1446 2 ECERNH3
21 100.0 1447 2 ECERNH3
22 100.0 1447 2 ECERNH3
23 100.0 1447 2 ECERNH3
24 100.0 1447 2 ECERNH3
25 100.0 1447 2 ECERNH3
26 100.0 1447 2 ECERNH3
27 100.0 1447 2 ECERNH3
28 100.0 1447 2 ECERNH3
29 100.0 1447 2 ECERNH3
30 100.0 1447 2 ECERNH3
31 100.0 1447 2 ECERNH3
32 100.0 1447 2 ECERNH3
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34 100.0 1447 2 ECERNH3
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36 100.0 1447 2 ECERNH3
37 100.0 1447 2 ECERNH3
38 100.0 1447 2 ECERNH3
39 100.0 1447 2 ECERNH3
40 100.0 1447 2 ECERNH3
41 100.0 1447 2 ECERNH3
42 100.0 1447 2 ECERNH3
43 100.0 1447 2 ECERNH3
44 100.0 1447 2 ECERNH3
45 100.0 1447 2 ECERNH3

ALIGNMENTS

RESULT 1
AX022152 25 bp CNA PAT 67-SEP-2000
DEFINITION Sequence 3 from Patent EP0957175
ACCESSION AX022152
VERSION AX022152.1 GI:10943828
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 25)
AUTHORS
TITLE
JOURNAL
ORIGIN
LOCATION/Qualifiers
SOURCE
1. 25
/db_xref="taxon:32644"
BASE COUNT 8 a 6 c 4 g 7 t
ORIGIN

Query Match 100.0% Score 25 DB 9 Length 25
Best Local Similarity 100.0% Pred. No. 2.3
Matches 25 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 gagcaagatattacttacc 25
|||||
DB 1 GAGCAAGATATTACTTACC 25

RESULT 2
105065

LOCUS 105065 41 bp
DEFINITION Sequence 11 from Patent EP 0241446
ACCESSION 105065
VERSION 105065.1 GI:591275
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 41)
AUTHORS
TITLE
JOURNAL
ORIGIN
BASE COUNT 12 a 11 c 5 t
ORIGIN

Query Match 100.0% Score 25 DB 10 Length 41
Best Local Similarity 100.0% Pred. No. 2.3
Matches 25 Conservative 0 Mismatches 0 Indels

QY 1 gagcaagatattacttacc 25
|||||
DB 1 GAGCAAGATATTACTTACC 25

RESULT 3
A1547 57 bp CNA PAT 67-SEP-2000
DEFINITION Hybridization probe number 4 for the detection of Esch.
ACCESSION A1547
VERSION A1547.1 GI:640868
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 57)
AUTHORS
TITLE
JOURNAL
ORIGIN
LOCATION/Qualifiers
SOURCE
1. 57
/db_xref="taxon:32644"
BASE COUNT 15 a 10 c 10 g 1 t
ORIGIN

Query Match 100.0% Score 25 DB 9 Length 57
Best Local Similarity 100.0% Pred. No. 2.3
Matches 25 Conservative 0 Mismatches 0 Indels

QY 1 gagcaagatattacttacc 25
|||||
DB 45 GAGCAAGATATTACTTACC 25

RESULT 4
190026 61 bp CNA PAT 67-SEP-2000
DEFINITION Sequence 7 from patent US 5723444
ACCESSION 190026
VERSION 190026.1 GI:3409966
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 61)
AUTHORS
Mabiat,C., Cros,P., Mandrand,B., Charles,M., Erout,M.

1	1	100.0	479	1	AB028373	Streptococcus
1	1	100.0	484	1	AB028356	Streptococcus
1	1	100.0	487	1	AB028339	Streptococcus
1	1	100.0	488	1	AB028343	Streptococcus
1	1	100.0	488	1	AB028342	Streptococcus
1	1	100.0	489	1	AB028372	Streptococcus
1	1	100.0	489	1	AB028329	Streptococcus
1	1	100.0	490	1	AB028340	Streptococcus
1	1	100.0	490	1	AB028342	Streptococcus
1	1	100.0	490	1	AB028357	Streptococcus
1	1	100.0	498	1	AB028345	Streptococcus
1	1	100.0	498	1	AB028340	Streptococcus
1	1	100.0	498	1	AB028372	Streptococcus
1	1	100.0	499	1	AB028342	Streptococcus
1	1	100.0	499	1	AB028343	Streptococcus
1	1	100.0	499	1	AB028348	Streptococcus
1	1	100.0	499	1	AB028350	Streptococcus
1	1	100.0	499	1	AB028358	Streptococcus
1	1	100.0	500	1	AB028362	Streptococcus
1	1	100.0	500	1	AB028326	Streptococcus
1	1	100.0	500	1	AB028347	Streptococcus
1	1	100.0	500	1	AB028361	Streptococcus
1	1	100.0	506	1	AB028349	Streptococcus
1	1	100.0	509	1	AB028372	Streptococcus
1	1	100.0	509	1	AB028376	Streptococcus
1	1	100.0	529	1	AB028376	Streptococcus

ALIGNMENTS

RESULT 1
 LOCUS AB042007 162 bp DNA
 DEFINITION Sequence 7 from Patent W-9705282
 ACCESSION AB042007
 VERSION AB042007.1 GI:7678780
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCES
 1 (bases 1 to 162)
 Pedraza, K.S., Haruta, S., and Pedro, M.S.,
 Denaturing Gradient Gel Electrophoresis Analysis of
 Community from Waste Ammonia with
 Unpublished (2000)
 2 (bases 1 to 162)
 Haruta, S. and Pedro, M.S.,
 Direct Submission
 Submitted (20-APP-2000) to the National Center for
 Human Genome Research, National Institutes of Health,
 Bethesda, MD, USA (E-mail: haruta@hgsr.nih.gov; haruta@hgsr.nih.gov)
 Tel: 301-358-4154; Fax: 301-358-4154

Query Match 100.0% Score 19 16 Length 162
 Best Local Similarity 100.0% P-Id No. 811
 Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 gtagcgccttccttcg 19
 DB 1 gtagcgccttccttcg 19

RESULT 2
 LOCUS AX022153
 DEFINITION Sequence 4 from Patent EP0957175-A
 ACCESSION AX022153
 VERSION AX022153.1 GI:10045827
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCES
 1 (bases 1 to 19)
 Method for the rapid detection of bacteria
 Patent: EP 0957175-A 4 17 NOV 1999
 GRONINGER ACAD ZIEKENHUIS (NL) ONIV GRONINGER (NL)
 LOCATION/Qualifiers
 1..19
 /organism="unidentified"
 /db_xref="taxon:12644"

Query Match 100.0% Score 19 16 Length 162
 Best Local Similarity 100.0% P-Id No. 811
 Matches 19: Conservative 0: Mismatches 0: Indels 0:

QY 1 gtagcgccttccttcg 19
 DB 1 gtagcgccttccttcg 19

RESULT 3
 LOCUS AB042007 162 bp DNA
 DEFINITION Sequence 7 from Patent W-9705282
 ACCESSION AB042007
 VERSION AB042007.1 GI:7678780
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCES
 1 (bases 1 to 162)
 Pedraza, K.S., Haruta, S., and Pedro, M.S.,
 Denaturing Gradient Gel Electrophoresis Analysis of
 Community from Waste Ammonia with
 Unpublished (2000)
 2 (bases 1 to 162)
 Haruta, S. and Pedro, M.S.,
 Direct Submission
 Submitted (20-APP-2000) to the National Center for
 Human Genome Research, National Institutes of Health,
 Bethesda, MD, USA (E-mail: haruta@hgsr.nih.gov; haruta@hgsr.nih.gov)
 Tel: 301-358-4154; Fax: 301-358-4154

Query Match 100.0% Score 19 16 Length 162
 Best Local Similarity 100.0% P-Id No. 811
 Matches 19: Conservative 0: Mismatches 0: Indels 0:

QY 1 gtagcgccttccttcg 19
 DB 1 gtagcgccttccttcg 19

Score: 18; DB 20; Length 1548;
Pred. No. 1.5; Mismatches 0; Indels 0; Gaps 0;

bacterium, isolate ST-11.

water: detection; flagellum;
glucose; carbon source;

ATUSHO KK.

of sea water - where oil contamination
microbe having properties from e.g.
am-negative bacterium, belonging to
on, etciz

for monitoring oil contamination of
sea water, a microbe having the following
lines; (2) it is a Gram-negative bacterium;
a gamma subdivision; (4) it cannot
carbon source; and (5) it efficiently
30C n-alkanes. This sequence represents
from the microbe of the invention,

497 G; 312 T; 0 other;

Score: 16.4; DB 20; Length 1529;
Pred. No. 11; Mismatches 1; Indels 0; Gaps 0;

DE Ras oncogene/LacZ reporter gene recombinant construct.
XX
KW Recombinant construct; rat; synapsin; promoter sequence; human
KW oncogene; ribosome binding site; reporter gene; beta-galactosidase
KW neuronal cell; transgenic animal; neuron; neuronal injury; ds.
XX
OS Synthetic.

FH Key
FT Promoter

Location/Qualifiers
1..1601
/tag- a
/note- "synapsin promoter"

FT CDS

1602..3288
/tag- b
/product- Ras oncogene product

FT RBS

3335..3920
/tag- c
/note- "internal ribosome entry site"

FT CDS

3921..6989
/tag- d
/product- beta-galactosidase

DE4325699-A.

PD 02-FEB-1995.

PF 30-JUL-1993; 93DE-4325699.

PR 30-JUL-1993; 93DE-4325699.

PA (BERN/) BERNIS H.

PI Berns H, Heumann R;

DR WPI: 1995-068046/10.

PT Recombinant DNA providing neuron specific expression of oncogene
PT and neuronal cells contg. them, used to identify cpts. with
PT neuron specific activity.

PS Disclosure: Fig 3; 15pp; German.

XX The nucleotide sequence of a novel recombinant construct comprising
CC rat synapsin gene promoter sequence linked to the genomic sequence of
CC human V-Ha-ras oncogene. These sequences are placed 5' to a fragment
CC containing an internal ribosome binding site and the structural sequence
CC for a reporter gene e.g. beta-galactosidase. The construct is an
CC of a vector that can be activated and transcribed specifically in
CC neuronal cells. The reporter gene is placed as a marker to determine
CC extent and localisation of the oncogene expression in the neuronal
CC animals) can be used to test compounds for neuron specific activity
CC compounds which cause neuronal injury.

SQ Sequence 6995 BP: 1489 A; 1964 C; 2022 G; 1490 T; 0 other;

Query Match 83.3%; Score 15; DB 16; Length 6995;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 15; Conservative 0; Mismatches 0; Indels 0;

OY 4 tccccctctgatgg 18
DB 1197 tccccctctgatgg 1183

RESULT 6
X83570/C
ID X83570 standard; DNA: 1528 BP.
AC X83570;
XX 21-DEC-1999 (first entry)

ALLEGEMENTS

RESULT	1
LOCUS	AX022156
DEFINITION	AX022156 19 bp cDNA PAT
ACCESSION	Sequence 7 from Patent EP0957175.
VERSION	AX022156
KEYWORDS	AX022156.1 GI:1045832
SOURCE	unidentified.
ORGANISM	unidentified
REFERENCE	unclassified.
AUTHORS	1 (bases 1 to 19)
TITLE	
JOURNAL	Method for the rapid determination of bacteria
FEATURES	Patent: EP 0957175-A 7 17-NOV-1999;
source	GONINGEN ACAP ZIEKENHUIS (NL); UNIV GONINGEN (NL).
	Location/Qualifiers
	1..19
	/organism="unidentified"
	/db_xref="taxon:32844"
BASE COUNT	1 a 4 g c 3 q 7 t
ORIGIN	

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Query Match      100.0%; Score 19;  DB 9;  Length 19;
Best Local Similarity 100.0%;  Pred. No. 12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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Gy	I	gcacatcctcttltccgg	19
Dh	I	gGACTCCTTTTTCGG	19

RESULT 2
AF145258/C

[illegible]

RESULT	1	3
ESL6SR/C		
LOCUS	EST6SRP	1440 bp LNA
DEFINITION	<i>Enterococcus</i> sp. (LMG2317) TSS RNA gene.	bct no
ACCESSION	X76177	
VERSION	X/6177.1 GI:517387	
KEYWORDS	16S ribosomal RNA.	
SOURCE	<i>Enterococcus</i> sp.	
ORGANISM	<i>Enterococcus</i> sp.	
	Bacteria; Firmicutes; Bacillus/ Clostridium group; End	
	<i>Enterococcus</i> .	
REFERENCE	1 (bases 1 to 1440)	
AUTHORS	Cai,J.	
TITLE	Direct Submission	
JOURNAL	Submitted (19-NOV-1993) J Cai, AFRC, Institute Food	
	Reading Laboratory, Earley Gate, Whiteknights Road, R	
	2EP, UK	
REFERENCE	2 (bases 1 to 1440)	
AUTHORS	Cai,J.,and Collins,M.D.	
JOURNAL	Unpublished	
FEATURES	Location/Qualifiers	
Source	I_1440	

IRRNA	<1	.>1440	
BASE COUNT	369 a	324 c	443 g
ORIGIN			259 t

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us-09-673-779-7.rge

100 3

Query Match 100.0% Score 19; DB 2; Length 1440;
Best Local Similarity 100.0% Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccactctcttttcg 19
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DB 32 gccactctcttttcg 14

RESULT 4
LOCUS EH18354 1445 bp DNA
DEFINITION Enterococcus hirae 16S rRNA gene.
ACCESSION Y18354
VERSION Y18354.1 GI:5578761
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE Enterococcus hirae.
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococaceae; Enterococcus.

REFERENCE 1 (bases 1 to 1445)
AUTHORS Lawson, P.A., Garbisa, S.E., Shah, H.N., Clark, D.F. and Collins, M.D.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1445)
AUTHORS Lawson, P.A.
TITLE Direct Submission
SUBMITTED (04-NOV-1998) P.A. Lawson, BBSRC Institute of Food Research, Reading Laboratory, Microbiology Dept., Earley Gate Whiteknights Road, Reading RG6 2PF UK
REMARK Revised by author

FEATURES
source Location/Qualifiers
1..1445
/organism="Enterococcus hirae"
/strain="NCFB 1258T"
/db_xref="taxon:1354"

rRNA

1..1445
/gene="16S rRNA"
/product="16S ribosomal RNA"
1..1445
/gene="16S rRNA"

BASE COUNT 368 a 338 c 434 g 305 t
ORIGIN

Query Match 100.0% Score 19; DB 2; Length 1445;
Best Local Similarity 100.0% Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gccactctcttttcg 19
|||||
DB 81 gccactctcttttcg 63

RESULT 5
LOCUS EH18294 1459 bp DNA
DEFINITION Enterococcus faecium 16S rRNA gene.
ACCESSION Y18294
VERSION Y18294.1 GI:5578754
KEYWORDS 16S ribosomal RNA; 16S rRNA gene.
SOURCE Enterococcus faecium.
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococaceae; Enterococcus.

REFERENCE 1 (bases 1 to 1459)
AUTHORS Lawson, P.A., Garbisa, S.E., Shah, H.N., Clark, D.F. and Collins, M.D.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1459)
AUTHORS Lawson, P.A.
TITLE Direct Submission
SUBMITTED (21-OCT-1998) P.A. Lawson, BBSRC Institute of Food Research, Reading Laboratory, Microbiology Dept., Earley Gate

REMARK Revised by author
FEATURES Location/Qualifiers
source 1..1459
/organism="Enterococcus faecium"
/strain="NCFB 942T"
/db_xref="taxon:1452"

rRNA

1..1459
/gene="16S rRNA"
/product="16S ribosomal RNA"
1..1459
/gene="16S rRNA"

BASE COUNT 372 a 344 c 439 g 305 t
ORIGIN

Query Match 100.0% Score 19; DB 2; Length 1440;
Best Local Similarity 100.0% Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0;

QY 1 gccactctcttttcg 19
|||||
DB 86 gccactctcttttcg 68

RESULT 6
LOCUS AF039901/c 1477 bp DNA
DEFINITION Enterococcus faecium 16S ribosomal RNA gene, partial
ACCESSION AF039901
VERSION AF039901.1 GI:2828124
KEYWORDS Enterococcus faecium.
SOURCE Enterococcus faecium.
ORGANISM Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcus.

REFERENCE

1 (bases 1 to 1477)
AUTHORS Patel, R., Piper, K.E., Kause, M.S., Steckelberg, M., Kohner, P., Hopkins, M.K., Cookerill, F.K. III and Kline, D.
TITLE Determination of 16S rRNA sequences of enterococci to species identification of nonmole Enterococcus isolates
JOURNAL J Clin. Microbiol. 36 (11): 1997-2007 (1997)

MEDLINE 98449879
2 (bases 1 to 1477)

AUTHORS Patel, R., Piper, K.E., Kause, M.S., Steckelberg, M., Kohner, P., Hopkins, M.K., Cookerill, F.K. and Kline, D.
TITLE Direct Submission
SUBMITTED (29-DEC-1997) Enterococcus Diseases Unit, Mayo Clinic, 200 First Street Southwest, Rochester

JOURNAL location/Qualifiers

FEATURES
source 1..1477
/organism="Enterococcus faecium"
/db_xref="taxon:1452"
/note="from 14 clinical isolates"
1..1477
/product="16S ribosomal RNA"

BASE COUNT 379 a 339 c 445 g 305 t
ORIGIN

Query Match 100.0% Score 19; DB 2; Length 1440;
Best Local Similarity 100.0% Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0;

QY 1 gccactctcttttcg 19
|||||
DB 66 gccactctcttttcg 48

RESULT 7
LOCUS AF061011/c 1507 bp DNA
DEFINITION Enterococcus faecium 16S rRNA gene, partial

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us-09-673-779-8.19e

3

gene 1.481
/gene="16S rRNA"
BASE COUNT 137 a 105 c 137 g 102 t
ORIGIN

Query Match 100.0% Score 19; DB 3; Length 481;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 gctaatgcagcgatcc 19
|||||
DB 214 gctaatgcagcgatcc 19g

RESULT 4
SH16SRND 771 bp DNA BCT 13-OCT-1993
LOCUS S.haemolyticus gene for 16S ribosomal RNA.
DEFINITION Z26896
VERSION Z26896.1 GI:407889
KEYWORDS 16S ribosomal RNA; ribosomal RNA.
SOURCE Staphylococcus haemolyticus.
ORGANISM Staphylococcus haemolyticus.
Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillaceae;
Staphylococcus.
REFERENCE 1 (bases 1 to 771)
AUTHORS Maclean, I.A. and Carter, P.E.
TITLE Phylogenetic analysis using 16S rRNA sequencing of Staphylococci
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 771)
AUTHORS Maclean, I.A.
TITLE Direct Submission
JOURNAL Submitted (11-OCT-1993) I. Maclean, University of Aberdeen,
Department of Medical Microbiology; Aberdeen, Scotland, UK
LOCATION/Qualifiers
FEATURES
source
1. 771
/organism="Staphylococcus haemolyticus"
/strain="TSM 20263"
/db_xref="taxon:1283"
1. 771
/product="16S ribosomal RNA"
BASE COUNT 214 a 159 c 236 g 162 t
ORIGIN

Query Match 100.0% Score 19; DB 3; Length 771;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 gctaatgcagcgatcc 19
|||||
DB 233 gctaatgcagcgatcc 215

RESULT 5
AF076030/c 1141 bp DNA BCT 09-SEP-1998
LOCUS Staphylococcus aureus 16S ribosomal RNA gene, partial sequence.
DEFINITION AF076030
VERSION AF076030.1 GI:551854
KEYWORDS Staphylococcus aureus.
SOURCE Staphylococcus aureus.
ORGANISM Staphylococcus aureus.
Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1 (bases 1 to 1141)
AUTHORS Okhravi, N., Adamson, P., Matheson, M.M., Towler, H.M.A. and
Lightham, S.
TITLE PCR-RFLP mediated diagnosis of bacteria in intraocular fluids from
patients with presumed bacterial endophthalmitis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1141)

AUTHORS Okhravi, N., Adamson, P., Matheson, M.M., Towler, H.M.A. and
Lightham, S.
TITLE Direct Submission
JOURNAL Submitted (01-MAY-1998) Department of Clinical Pathology,
Institute of Ophthalmology, 11-43 Bath Street, London
LOCATION/Qualifiers
FEATURES
source
1. 1141
/organism="Staphylococcus aureus"
/db_xref="taxon:1283"
/note="ocular isolate from a patient with
endophthalmitis"
1. 1141
/product="16S ribosomal RNA"
BASE COUNT 307 a 247 c 338 g 249 t
ORIGIN

Query Match 100.0% Score 19; DB 1; Length 1141;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0

QY 1 gctaatgcagcgatcc 19
|||||
DB 213 gctaatgcagcgatcc 195

RESULT 6
AF107307/c 1309 bp DNA BCT 12-
LOCUS Staphylococcus aureus subsp. aureus 16S ribosomal
DEFINITION partial sequence.
VERSION AF107307
KEYWORDS AF107307.1 GI:4406246
SOURCE Staphylococcus aureus subsp. aureus.
ORGANISM Staphylococcus aureus subsp. aureus.
Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
REFERENCE 1 (bases 1 to 1309)
AUTHORS Miller, K., Agerholm, J.S., Agerholm, N. and
TITLE Abscess disease, caseous lymphadenitis and pneumonia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1309)
AUTHORS Ahrens, P.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-1998) Mørkved, J., Danish Veterinary
Bulowvej 27, Copenhagen, DK-1795, Denmark
LOCATION/Qualifiers
FEATURES
source
1. 1309
/organism="Staphylococcus aureus subsp. aureus"
/strain="4"
/sub-species="aureus"
/db_xref="taxon:1279"
/note="isolated from sheep"
1. 1309
/product="16S ribosomal RNA"
BASE COUNT 360 a 280 c 373 g 295 t
ORIGIN

Query Match 100.0% Score 19; DB 1; Length 1309;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0

QY 1 gctaatgcagcgatcc 19
|||||
DB 144 gctaatgcagcgatcc 126

RESULT 7
AF146368/c 1350 bp DNA BCT 17-
LOCUS

Wed May 9 10:10:44 2001

us-09-673-779-9.rge

ORIGIN

Query Match 100.0% Score 181 DB 92 Length 555
Best Local Similarity 100.0% Prod. No. 44
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

U7 1 ccgaagggaagctcta 18
|||||
DB 49 ccgaagggaagctcta 32

RESULT 4

A32071/c 55 bp DNA PAT 08-DEC-1995
LOCUS A32071 DNA probe (S. aureus) from patent EP0395292.
DEFINITION A32071
ACCESSION A32071 GI:1249526
VERSION A32071.1 GI:1249526
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 55)
AUTHORS Barry, T.G., Gannon, B. X. and Powell, L.R.
TITLE Generation of specific probes for target nucleotide sequences
JOURNAL Patent: EP 0395292-A 46 31-OCT-1990;

REFERENCE 1 (bases 1 to 55)
AUTHORS Barry, T.G., Gannon, B. X. and Powell, L.R.
TITLE Generation of specific probes for target nucleotide sequences
JOURNAL Patent: EP 0395292-A 46 31-OCT-1990;

REFERENCE 1 (bases 1 to 55)
AUTHORS Barry, T.G., Gannon, B. X. and Powell, L.R.
TITLE Generation of specific probes for target nucleotide sequences
JOURNAL Patent: EP 0395292-A 46 31-OCT-1990;

FEATURES
SOURCE Location/Qualifiers

BASE COUNT 17 a 15 c 9 g 14 t
ORIGIN

Query Match 100.0% Score 181 DB 92 Length 555
Best Local Similarity 100.0% Prod. No. 44
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

U7 1 ccgaagggaagctcta 18
|||||
DB 49 ccgaagggaagctcta 32

RESULT 5
AF102128/c 481 bp DNA BCI 22-APR-1999
LOCUS AF102128 uncultured bacterium 5744rev 16S ribosomal RNA gene, partial
DEFINITION AF102128
ACCESSION AF102128 GI:4633105
VERSION AF102128
KEYWORDS uncultured bacterium 5744rev.
SOURCE uncultured bacterium 5744rev.
ORGANISM Bacteria; environmental samples.

REFERENCE 1 (bases 1 to 481)
AUTHORS Riley, D.E. and Krieger, J.N.
TITLE Bacterial DNA in tissue from men with chronic prostatitis
JOURNAL Unpublished
AUTHORS 2 (bases 1 to 481)
Riley, D.E. and Krieger, J.N.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1998) University of Washington (VMAC),
Campus Box 356510, Seattle, WA 98195, USA
Location/Qualifiers

FEATURES
SOURCE 1. 481

/specific host "Homo sapiens"
/db_xref="taxon:9606"
/clone="5744rev"
/note="RNA cloned from tissue of cultured patient"
patient"
GI: 4633105
/product="16S ribosomal RNA"
DB 481 CCGAAGGGGAAGCTCTA 464

Query Match 100.0% Score 181 DB 92 Length 555
Best Local Similarity 100.0% Prod. No. 44
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

U7 1 ccgaagggaagctcta 18
|||||
DB 125 CCGAAGGGGAAGCTCTA 108

RESULT 6

AF041357/c 924 bp DNA BCI
LOCUS AF041357 Staphylococcus xylosum 16S ribosomal RNA gene, partial
DEFINITION AF041357
ACCESSION AF041357 GI:3095090
VERSION AF041357.1 GI:3095090
KEYWORDS
SOURCE Staphylococcus xylosum.
ORGANISM Staphylococcus xylosum.
REFERENCE 1 (bases 1 to 924)
AUTHORS Gory, L., Millet, L., Godard, J., Montel, M.-C., and J.
TITLE Specific detection of Staphylococcus isolated from
JOURNAL fluorescent in situ hybridization with 16S rRNA-targeted
oligonucleotide probes

REFERENCE 1 (bases 1 to 924)
AUTHORS Gory, L., Millet, L., Godard, J., Montel, M.-C., and J.
TITLE Specific detection of Staphylococcus isolated from
JOURNAL fluorescent in situ hybridization with 16S rRNA-targeted
oligonucleotide probes

REFERENCE 1 (bases 1 to 924)
AUTHORS Gory, L., Millet, L., Godard, J., Montel, M.-C., and J.
TITLE Specific detection of Staphylococcus isolated from
JOURNAL fluorescent in situ hybridization with 16S rRNA-targeted
oligonucleotide probes

REFERENCE 1 (bases 1 to 924)
AUTHORS Gory, L., Millet, L., Godard, J., Montel, M.-C., and J.
TITLE Specific detection of Staphylococcus isolated from
JOURNAL fluorescent in situ hybridization with 16S rRNA-targeted
oligonucleotide probes

FEATURES
SOURCE

BASE COUNT 244 a 206 c 248 g 204 t
ORIGIN

Query Match 100.0% Score 181 DB 92 Length 555
Best Local Similarity 100.0% Prod. No. 44
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

U7 1 ccgaagggaagctcta 18
|||||
DB 481 CCGAAGGGGAAGCTCTA 464

RESULT 7

AF041363/c 938 bp DNA BCI
LOCUS AF041363 Staphylococcus equorum 16S ribosomal RNA gene, partial
DEFINITION AF041363
ACCESSION AF041363 GI:3095096
VERSION AF041363.1 GI:3095096
KEYWORDS Staphylococcus equorum.
SOURCE Staphylococcus equorum.
ORGANISM Staphylococcus equorum.
REFERENCE 1 (bases 1 to 938)
AUTHORS Gory, L., Millet, L., Godard, J., Montel, M.-C., and J.
TITLE Specific detection of Staphylococcus isolated from
JOURNAL fluorescent in situ hybridization with 16S rRNA-targeted
oligonucleotide probes

[illegible]

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RESULT 3
A32065/c A32065 80 bp DNA PAT
LOCUS A32065 80 bp DNA Probe (S. aureus) FROM Patent EP0395292.
ACCESSION A32065
VERSION A32065.1 GI:1243520
KEYWORDS
SCORE
ORGANISM
REFERENCE
1 (bases 1 to 80)
AUTHORS Barry, T. O., Gannon, B. X. and Powell, B.
TITLE Generation of specific probes for target nucleotide se-
JOURNAL Patent: EP 0395292-A 40 31-Oct-1990
Barry, Thomas Gerard; Gannon, Bernard Francis Xavier;
IRELAND; Powell, Richard; UNIVERSITY COLLEGE GALWAY;
Gerard, Gannon, Bernard Francis Xavier; BIOSEARCH, I
Gannon, Bernard Francis Xavier; BOLAS (trading as Bio
Ireland) - The Irish Science and Technology Agency;
Richard; UNIVERSITY COLLEGE GALWAY
Location/Qualifiers
1. 80
/organism="Synthetic Construct"
/ld_xref="taxon:12210"
BASE COUNT 20 a 19 c 25 t
ORIGIN
Query Match 100.0%; Score 24; Len 9; Ident. 9;
Best Local Similarity 100.0%; Pctd. No. 3;
Matches 24; Conservative 0; Mismatches 0; Indels
0
1 agagaagcaagcttcgcgcgtt 24
|||||
71 AGAGAGCAAGCAAGCTTCGTCGCTT 48

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